

0590
0808 #14

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RAW SEQUENCE LISTING

DATE: 08/12/2002

PATENT APPLICATION: US/10/000,151B

TIME: 09:42:25

Input Set : A:\HERG-KCR1rev1.ST25.txt

Output Set: N:\CRF4\08122002\J000151B.raw

3 <110> APPLICANT: Balser, Jeffrey R.
 4 George, Alfred L.
 6 <120> TITLE OF INVENTION: HUMAN KCRI REGULATION OF HERG POTASSIUM CHANNEL BLOCK
 8 <130> FILE REFERENCE: Vanderbilt Ref No. VU0120; Attorney Docket No. 1242-49
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/000,151B
 11 <141> CURRENT FILING DATE: 2000-10-30
 13 <160> NUMBER OF SEQ ID NOS: 5
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1857
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: misc_feature
 24 <222> LOCATION: (1)..(1857)
 25 <223> OTHER INFORMATION: n is any nucleic acid
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1422)
 31 <223> OTHER INFORMATION: n is any nucleic acid
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 39 ttt tta gtg tcc tgc ctc ctc ttc tcc gcc ttc agc cgg gcg ctg cga 96
 40 Phe Leu Val Ser Cys Leu Leu Phe Ser Ala Phe Ser Arg Ala Leu Arg
 41 20 25 30
 43 gag ccc tac atg gac gag atc ttc cac ctg cct cag gcg cag cgc tac 144
 44 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
 45 35 40 45
 47 tgt gag ggc cat ttc tcc ctt tcc cag tgg gat ccc atg att act aca 192
 48 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
 49 50 55 60
 51 tta cct ggc ttg tac ctg gtg tca gtt gga gtg gtc aaa cct gcc att 240
 52 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
 53 65 70 75 80
 55 tgg atc ttt gga tgg tct gaa cat gtt gtc tgc tcc att ggg atg ctc 288
 56 Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu
 57 85 90 95
 59 aga ttt gtt aat ctt ctc ttc agt gtt ggc aac ttc tat tta cta tat 336
 60 Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr
 61 100 105 110
 63 ttg ctt ttc cac aag gta caa ccc aga aac aag gct gcc tca agt atc 384

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64	Leu	Leu	Phe	His	Lys	Val	Gln	Pro	Arg	Asn	Lys	Ala	Ala	Ser	Ser	Ile	
65			115					120					125				
67	cag	aga	gtc	ttg	tca	aca	tta	aca	cta	gca	gta	ttt	cca	aca	ctt	tat	432
68	Gln	Arg	Val	Leu	Ser	Thr	Leu	Thr	Leu	Ala	Val	Phe	Pro	Thr	Leu	Tyr	
69		130						135				140					
71	ttt	ttt	aac	ttc	ctt	tat	tat	aca	gaa	gca	gga	tct	atg	ttt	ttt	act	480
72	Phe	Phe	Asn	Phe	Leu	Tyr	Thr	Glu	Ala	Gly	Ser	Met	Phe	Phe	Thr		
73	145					150					155					160	
75	ctt	ttt	gca	tat	ttg	atg	tgt	ctt	tat	gga	aat	cat	aaa	act	tca	gcc	528
76	Leu	Phe	Ala	Tyr	Leu	Met	Cys	Leu	Tyr	Gly	Asn	His	Lys	Thr	Ser	Ala	
77					165					170				175			
79	ttc	ctt	gga	ttt	tgt	ggc	ttc	atg	ttt	cgg	caa	aca	aat	atc	atc	tgg	576
80	Phe	Leu	Gly	Phe	Cys	Gly	Phe	Met	Phe	Arg	Gln	Thr	Asn	Ile	Ile	Trp	
81				180					185					190			
83	gct	gtc	ttc	tgt	gca	ggg	aat	gtc	att	gca	caa	aag	tta	act	gag	gct	624
84	Ala	Val	Phe	Cys	Ala	Gly	Asn	Val	Ile	Ala	Gln	Lys	Leu	Thr	Glu	Ala	
85			195					200					205				
87	tgg	aaa	act	gag	cta	caa	aag	aag	gaa	gac	aga	ctt	cca	cct	att	aaa	672
88	Trp	Lys	Thr	Glu	Leu	Gln	Lys	Lys	Glu	Asp	Arg	Leu	Pro	Pro	Ile	Lys	
89		210					215					220					
91	gga	cca	ttt	gca	gaa	ttc	aga	aaa	att	ctt	cag	ttt	ctt	ttg	gct	tat	720
92	Gly	Pro	Phe	Ala	Glu	Phe	Arg	Lys	Ile	Leu	Gln	Phe	Leu	Leu	Ala	Tyr	
93	225				230						235					240	
95	tcc	atg	tcc	ttt	aaa	aac	ttg	agt	atg	ctt	ttc	tgt	ttg	act	tgg	ccc	768
96	Ser	Met	Ser	Phe	Lys	Asn	Leu	Ser	Met	Leu	Phe	Cys	Leu	Thr	Trp	Pro	
97				245						250				255			
99	tac	atc	ctt	ctg	gga	ttt	ctg	ttt	tgt	gct	ttt	gta	gta	gtt	aat	ggt	816
100	Tyr	Ile	Leu	Leu	Gly	Phe	Leu	Phe	Cys	Ala	Phe	Val	Val	Val	Asn	Gly	
101			260						265					270			
103	gga	att	gtt	att	ggc	gat	cgg	agt	agt	cat	gaa	gcc	tgt	ctt	cat	ttt	864
104	Gly	Ile	Val	Ile	Gly	Asp	Arg	Ser	Ser	His	Glu	Ala	Cys	Leu	His	Phe	
105			275					280					285				
107	cct	caa	cta	ttc	tac	ttt	ttt	tca	ttt	act	ctc	ttt	ttt	tct	ttt	cct	912
108	Pro	Gln	Leu	Phe	Tyr	Phe	Phe	Ser	Phe	Thr	Leu	Phe	Phe	Ser	Phe	Pro	
109		290					295					300					
111	cat	ctc	ctg	tct	cct	agc	aaa	att	aag	act	ttt	ctt	tcc	tta	gtt	tgg	960
112	His	Leu	Leu	Ser	Pro	Ser	Lys	Ile	Lys	Thr	Phe	Leu	Ser	Leu	Val	Trp	
113	305					310					315				320		
115	aaa	cat	gga	att	ctg	ttt	ttg	gtg	gtt	acc	tta	gtc	tct	gtg	ttt	tta	1008
116	Lys	His	Gly	Ile	Leu	Phe	Leu	Val	Val	Thr	Leu	Val	Ser	Val	Phe	Leu	
117				325						330				335			
119	gtt	tgg	aaa	ttc	act	tat	gct	cat	aaa	tac	ttg	cta	gca	gac	aat	aga	1056
120	Val	Trp	Lys	Phe	Thr	Tyr	Ala	His	Lys	Tyr	Leu	Leu	Ala	Asp	Asn	Arg	
121			340						345					350			
123	cat	tat	act	ttc	tat	gtg	tgg	aaa	aga	gtt	ttt	caa	aga	tat	gca	att	1104
124	His	Tyr	Thr	Phe	Tyr	Val	Trp	Lys	Arg	Val	Phe	Gln	Arg	Tyr	Ala	Ile	
125			355					360					365				
127	ctg	aaa	tat	ttg	tta	gtt	cca	gcc	tat	ata	ttt	gct	ggt	tgg	agt	ata	1152
128	Leu	Lys	Tyr	Leu	Leu	Val	Pro	Ala	Tyr	Ile	Phe	Ala	Gly	Trp	Ser	Ile	

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Input Set : A:\HERG-KCRLrev1.ST25.txt

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132 Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe
133 385      390      395      400
135 ata tgc ttg ttc att gtt ata gtt cct cag aaa ctg ctg gaa ttt cgt      1248
136 Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg
137      405      410      415
139 tac ttc att tta cct tat gtc att tat agg ctt aac ata act ctg cct      1296
140 Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro
141      420      425      430
143 ccc aca tcc aga ctt gtt tgt gaa ctg agt tgc tat gca att gtt aat      1344
144 Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn
145      435      440      445
147 ttc ata act ttt tac atc ttt ctg aac aag act ttt cag tgg cca aat      1392
148 Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn
149      450      455      460
151 agt cag gac att caa agg ttt atg tgg taa tatcagtgat attttgaact      1442
152 Ser Gln Asp Ile Gln Arg Phe Met Trp
153 465      470
W--> 155 gtaaaaatgg acttaataat agaccatttc tacaaagaac aactgaatag gnggaaaaca      1502
157 tgggaatttct tttaggtgca gtggtggtct tcaaattaca ttagtttttt taatatatat      1562
159 tttaaacata tgtaagaaat taagtggcaa agaactggga aagcttaaga cctgcttcaa      1622
W--> 161 angcctgaat aatgggaaaa taaanwngtt tncagatatc tcatatcgct cnnknatgn      1682
W--> 163 tggcccytmn caangcttgg gaatgkttnn wntgnataag ttnattaaan ctggggnntgc      1742
W--> 165 tnnmwatnac ttnnkncca nccwmnnwac natgmnntan nnantattta caaaggctcag      1802
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175 <220> FEATURE:
176 <221> NAME/KEY: misc_feature
177 <222> LOCATION: (1)..(1857)
178 <223> OTHER INFORMATION: n is any nucleic acid
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187      20      25      30
190 Glu Pro Tyr Met Asp Glu Ile Phe His Leu Pro Gln Ala Gln Arg Tyr
191      35      40      45
194 Cys Glu Gly His Phe Ser Leu Ser Gln Trp Asp Pro Met Ile Thr Thr
195      50      55      60
198 Leu Pro Gly Leu Tyr Leu Val Ser Val Gly Val Val Lys Pro Ala Ile
199 65      70      75      80
202 Trp Ile Phe Gly Trp Ser Glu His Val Val Cys Ser Ile Gly Met Leu
203      85      90      95
206 Arg Phe Val Asn Leu Leu Phe Ser Val Gly Asn Phe Tyr Leu Leu Tyr
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210 Leu Leu Phe His Lys Val Gln Pro Arg Asn Lys Ala Ala Ser Ser Ile
211      115      120      125
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215      130      135      140
218 Phe Phe Asn Phe Leu Tyr Tyr Thr Glu Ala Gly Ser Met Phe Phe Thr
219 145      150      155      160
222 Leu Phe Ala Tyr Leu Met Cys Leu Tyr Gly Asn His Lys Thr Ser Ala
223      165      170      175
226 Phe Leu Gly Phe Cys Gly Phe Met Phe Arg Gln Thr Asn Ile Ile Trp
227      180      185      190
230 Ala Val Phe Cys Ala Gly Asn Val Ile Ala Gln Lys Leu Thr Glu Ala
231      195      200      205
234 Trp Lys Thr Glu Leu Gln Lys Lys Glu Asp Arg Leu Pro Pro Ile Lys
235      210      215      220
238 Gly Pro Phe Ala Glu Phe Arg Lys Ile Leu Gln Phe Leu Leu Ala Tyr
239 225      230      235      240
242 Ser Met Ser Phe Lys Asn Leu Ser Met Leu Phe Cys Leu Thr Trp Pro
243      245      250      255
246 Tyr Ile Leu Leu Gly Phe Leu Phe Cys Ala Phe Val Val Val Asn Gly
247      260      265      270
250 Gly Ile Val Ile Gly Asp Arg Ser Ser His Glu Ala Cys Leu His Phe
251      275      280      285
254 Pro Gln Leu Phe Tyr Phe Phe Ser Phe Thr Leu Phe Phe Ser Phe Pro
255      290      295      300
258 His Leu Leu Ser Pro Ser Lys Ile Lys Thr Phe Leu Ser Leu Val Trp
259 305      310      315      320
262 Lys His Gly Ile Leu Phe Leu Val Val Thr Leu Val Ser Val Phe Leu
263      325      330      335
266 Val Trp Lys Phe Thr Tyr Ala His Lys Tyr Leu Leu Ala Asp Asn Arg
267      340      345      350
270 His Tyr Thr Phe Tyr Val Trp Lys Arg Val Phe Gln Arg Tyr Ala Ile
271      355      360      365
274 Leu Lys Tyr Leu Leu Val Pro Ala Tyr Ile Phe Ala Gly Trp Ser Ile
275      370      375      380
278 Ala Asp Ser Leu Lys Ser Lys Pro Ile Phe Trp Asn Leu Met Phe Phe
279 385      390      395      400
282 Ile Cys Leu Phe Ile Val Ile Val Pro Gln Lys Leu Leu Glu Phe Arg
283      405      410      415
286 Tyr Phe Ile Leu Pro Tyr Val Ile Tyr Arg Leu Asn Ile Thr Leu Pro
287      420      425      430
290 Pro Thr Ser Arg Leu Val Cys Glu Leu Ser Cys Tyr Ala Ile Val Asn
291      435      440      445
294 Phe Ile Thr Phe Tyr Ile Phe Leu Asn Lys Thr Phe Gln Trp Pro Asn
295      450      455      460
298 Ser Gln Asp Ile Gln Arg Phe Met Trp
299 465      470
302 <210> SEQ ID NO: 3
303 <211> LENGTH: 1159
304 <212> TYPE: PRT

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Output Set: N:\CRF4\08122002\J000151B.raw

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305 <213> ORGANISM: Homo sapiens
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314 20 25 30
317 Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe
318 35 40 45
321 Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys
322 50 55 60
325 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala
326 65 70 75 80
329 Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile
330 85 90 95
333 Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val
334 100 105 110
337 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn
338 115 120 125
341 Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp
342 130 135 140
345 Thr Asn His Arg Gly Pro Thr Ser Trp Leu Ala Pro Gly Arg Ala
346 145 150 155 160
349 Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala Arg
350 165 170 175
353 Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Gly Ala Pro Gly
354 180 185 190
357 Ala Val Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser Glu
358 195 200 205
361 Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala Gly
362 210 215 220
365 Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser Pro
366 225 230 235 240
369 Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser Leu
370 245 250 255
373 Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg Ser
374 260 265 270
377 Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp Ile
378 275 280 285
381 Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Pro Arg His Ala Ser
382 290 295 300
385 Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr Ser
386 305 310 315 320
389 Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln Ile
390 325 330 335
393 Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser Pro
394 340 345 350
397 Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr His
398 355 360 365
401 Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/12/2002
PATENT APPLICATION: US/10/000,151B TIME: 09:42:26

Input Set : A:\HERG-KCR1rev1.ST25.txt
Output Set: N:\CRF4\08122002\J000151B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1494,1624,1647,1649,1654,1674,1675,1676,1678,1682,1692,1696

Seq#:1; N Pos. 1711,1712,1714,1717,1725,1732,1738,1739,1744,1745,1750,1755

Seq#:1; N Pos. 1756,1757,1759,1763,1767,1768,1769,1773,1777,1778,1779,1782

Seq#:1; N Pos. 1783,1784,1786,1830,1849,1853

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1442
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1622
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1682
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1742
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1802